

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/566,941
Source: FWP
Date Processed by STIC: 2/9/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 02/09/2006

PATENT APPLICATION: US/10/566,941

TIME: 14:10:57

Input Set : A:\11916.0058.PCUS02.ST25.txt

Output Set: N:\CRF4\02012006\J566941.raw

3 <110> APPLICANT: Dyer, Cheryl J.
 4 Du, Fengxing
 5 Grosz, Michael D.
 6 Byatt, John C.
 8 <120> TITLE OF INVENTION: USE OF A SINGLE NUCLEOTIDE POLYMORPHISM IN THE CODING REGION
 OF
 9 THE LEPTIN RECEPTOR GENE TO ENHANCE PORK PRODUCTION
 11 <130> FILE REFERENCE: 11916.0058.PCUS02
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/566,941
 C--> 13 <141> CURRENT FILING DATE: 2006-02-02
 13 <150> PRIOR APPLICATION NUMBER: US. 60/553,582
 14 <151> PRIOR FILING DATE: 2004-03-16
 16 <150> PRIOR APPLICATION NUMBER: U.S. 60/493,158
 17 <151> PRIOR FILING DATE: 2003-08-07
 19 <160> NUMBER OF SEQ ID NOS: 44
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 21
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Synthetic nucleotide
 31 <400> SEQUENCE: 1
 32 atgatgaggc agttgttgca a 21
 35 <210> SEQ ID NO: 2
 36 <211> LENGTH: 20
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Artificial Sequence
 40 <220> FEATURE:
 41 <223> OTHER INFORMATION: Synthetic nucleotide
 43 <400> SEQUENCE: 2
 44 ccttcctgc aatgttgtct 20
 47 <210> SEQ ID NO: 3
 48 <211> LENGTH: 773
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Sus scrofa
 52 <400> SEQUENCE: 3
 53 gtggggttaag gacctgatgt tgtcactact atggctcgag tcaactgctgg ggcattgagtt 60
 55 tgatccctgg tcctggaaat tcacatgctg tgcattgtggc catatatata tgtatgtatg 120
 57 tgtatatata tacactcaca tacatgtata tatatatatg tgagtgtata tatatatatta 180
 59 tgatgtcaaa ttaatgggga aaataaaatg tgaatttcta aaaaggggtg cttaaagagtg 240
 61 gcattatctc taagggtata tgctccctct taagtataac actttggaca atggaagagc 300
 63 tttgtattag gcactgtttg agcacttgga aagttaaata attattgttg aagactgcat 360
 65 gttttaatct tagatacttc ctatttatgt cttagtcaaa atgattaatt gcttttctat 420

(pg. 6)

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67 gtgtctttta aatgtcctaa cagaatttat ttatgtgata actgcatttg acttggcata      480
69 tccaattact ccttggaaat ttaagttgtc ttgcatgcca ccaaatacaa catatgactt      540
71 cctcttgccct gctggaatct caaagaacac ttcaactttg aatggacatg atgaggcagt      600
73 tgttgaaacg gaacttaatt caagtgttac ctacttatca aacttatctt ctaaaacaac      660
75 tttccactgt tgcttttgga gtgaggaaga taaaaactgc tctgtacatg cagacaacat      720
77 tgcagggaag gcatttgttt cagcagtaaa ttccttagtt tttcaacaaa cag              773
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81 <211> LENGTH: 20
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
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86 <223> OTHER INFORMATION: Synthetic nucleotide
88 <400> SEQUENCE: 4
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98 <223> OTHER INFORMATION: Synthetic nucleotide
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104 <210> SEQ ID NO: 6
105 <211> LENGTH: 25
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107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Synthetic nucleotide
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117 <211> LENGTH: 30
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: Synthetic nucleotide
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125 gtggaaagtt gttttagaag ataagtttga                    30
128 <210> SEQ ID NO: 8
129 <211> LENGTH: 16
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Synthetic nucleotide
136 <400> SEQUENCE: 8
137 tgttgaaacg gaactt                                16
140 <210> SEQ ID NO: 9
141 <211> LENGTH: 17
142 <212> TYPE: DNA

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146 <223> OTHER INFORMATION: Synthetic nucleotide
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153 <211> LENGTH: 421
154 <212> TYPE: DNA
155 <213> ORGANISM: Sus scrofa
158 <220> FEATURE:
159 <221> NAME/KEY: CDS
160 <222> LOCATION: (133)..(420)
162 <220> FEATURE:
163 <221> NAME/KEY: misc_feature
164 <222> LOCATION: (299)..(299)
165 <223> OTHER INFORMATION: N = T or C
167 <220> FEATURE:
168 <221> NAME/KEY: misc_feature
169 <222> LOCATION: (310)..(310)
170 <223> OTHER INFORMATION: N = T or A
172 <220> FEATURE:
173 <221> NAME/KEY: misc_feature
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175 <223> OTHER INFORMATION: N = T or C
177 <400> SEQUENCE: 10
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180 tagatacttc ctatttatgt cttagtcaaa atgattaatt gcttttctat gtgtctttta      120
182 aatgtcctaa ca gaa ttt att tat gtg ata act gca ttt gac ttg gca tat      171
183           Glu Phe Ile Tyr Val Ile Thr Ala Phe Asp Leu Ala Tyr
184           1           5           10
186 cca att act cct tgg aaa ttt aag ttg tct tgc atg cca cca aat aca      219
187 Pro Ile Thr Pro Trp Lys Phe Lys Leu Ser Cys Met Pro Pro Asn Thr
188       15           20           25
190 aca tat gac ttc ctc ttg cct gct gga atc tca aag aac act tca act      267
191 Thr Tyr Asp Phe Leu Leu Pro Ala Gly Ile Ser Lys Asn Thr Ser Thr
192 30           35           40           45
W--> 194 ttg aat gga cat gat gag gca gtt gtt gaa ang gaa ctt aat nna agt      315
195 Leu Asn Gly His Asp Glu Ala Val Val Glu Xaa Glu Leu Asn Xaa Ser
196           50           55           60
198 ggt acc tac tta tca aac tta tct tct aaa aca act ttc cac tgt tgc      363
199 Gly Thr Tyr Leu Ser Asn Leu Ser Ser Lys Thr Thr Phe His Cys Cys
200           65           70           75
202 ttt tgg agt gag gaa gat aaa aac tgc tct gta cat gca gac aac att      411
203 Phe Trp Ser Glu Glu Asp Lys Asn Cys Ser Val His Ala Asp Asn Ile
204           80           85           90
206 gca ggg aag g                                     421
207 Ala Gly Lys
208           95
211 <210> SEQ ID NO: 11

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Input Set : A:\11916.0058.PCUS02.ST25.txt

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212 <211> LENGTH: 96
 213 <212> TYPE: PRT
 214 <213> ORGANISM: Sus scrofa
 216 <220> FEATURE:
 217 <221> NAME/KEY: misc_feature
 218 <222> LOCATION: (56)..(56)
 219 <223> OTHER INFORMATION: The 'Xaa' at location 56 stands for Lys, Arg, Thr, or Met.
 221 <220> FEATURE:
 222 <221> NAME/KEY: misc_feature
 223 <222> LOCATION: (60)..(60)
 224 <223> OTHER INFORMATION: The 'Xaa' at location 60 stands for Lys, Arg, Thr, Ile, Glu,
 Gly,
 225 Ala, Val, Gln, Pro, Leu, or Ser.
 227 <400> SEQUENCE: 11
 229 Glu Phe Ile Tyr Val Ile Thr Ala Phe Asp Leu Ala Tyr Pro Ile Thr
 230 1 5 10 15
 233 Pro Trp Lys Phe Lys Leu Ser Cys Met Pro Pro Asn Thr Thr Tyr Asp
 234 20 25 30
 237 Phe Leu Leu Pro Ala Gly Ile Ser Lys Asn Thr Ser Thr Leu Asn Gly
 238 35 40 45
 W--> 241 His Asp Glu Ala Val Val Glu Xaa Glu Leu Asn Xaa Ser Gly Thr Tyr
 242 50 55 60
 245 Leu Ser Asn Leu Ser Ser Lys Thr Thr Phe His Cys Cys Phe Trp Ser
 246 65 70 75 80
 249 Glu Glu Asp Lys Asn Cys Ser Val His Ala Asp Asn Ile Ala Gly Lys
 250 85 90 95
 253 <210> SEQ ID NO: 12
 254 <211> LENGTH: 4050
 255 <212> TYPE: DNA
 256 <213> ORGANISM: Sus scrofa
 258 <400> SEQUENCE: 12
 259 cttctctgaa gtaagatgac gtgtccaaag ttctctgtgg ctttgttaca ttgggaattt 60
 261 atttatgtga taactgcatt tgacttggca tatccaatta ctcttggaa atttaagttg 120
 263 tcttgcacgc caccaaatac aacatatgac ttctcttgc ctgctggaat ctcaaagaac 180
 265 acttcaactt tgaatggaca tgatgaggca gttgttgaaa cggaacttaa tataagtggg 240
 267 acctacttat caaactttatc ttctaaaaca actttccact gttgcttttg gagtgaggaa 300
 269 gataaaaact gctctgtaca tgcagacaac attgcaggggaggcatttgt ttcagcagta 360
 271 aattccttag tttttcaaca aacaggtgca aactggaaca tacagtgtg gatgaaagag 420
 273 gacttgaaat tattcatctg ttatatggag tcattattta agaatcctt caagaattat 480
 275 gaccttaaag ttcattcttt atatgttctg ctggaagtgt tagaaggatc acctctgtctc 540
 277 cccagaaaag gtagttttca gagcgttcaa tgcaactgca gtgctcgtga atgttgtgaa 600
 279 tgccatgtgc ctgtgtcggc agccaaactc aactacaccc ttcttatgta ttgaaaatc 660
 281 acatctggtg gagcagtttt tcaactcacct ctcatgtcag ttcagcccat aaacgttgtg 720
 283 aagcctgac caccattagg tttgcatatg gaaatcacag aactggtaa tttaaagatt 780
 285 tcttgggtcca gcccaacact ggtaaccattt caacttcaat atcaagtaaa atattcagag 840
 287 aattctacaa caaatatgag agaagctgat gagatcgtct cagatacatc tctgcttgta 900
 289 gacagtgtgc ttcccgggtc ttcatatgag gttcaggtga ggggcaagag actggatggc 960
 291 ccaggaatct ggagtgtgct gagcaccctt tttactttta ccacacaaga tggtatatac 1020
 293 tttccacctt aaattctgac aagtgttggg tctaacattt cttttcactg catctataaa 1080
 295 aatgagaaca agatcgtttc ctcaaaaaag attgtttggt ggatgaattt agctgagaag 1140

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Input Set : A:\11916.0058.PCUS02.ST25.txt

Output Set: N:\CRF4\02012006\J566941.raw

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297 attcctcaaa gtcagtatga tgttgtgggt gaccatgtta gcaaagtcac ttttcccaat 1200
299 atgaatgcaa ccaaacctcg aggaaagtgc acctatgatg cagtgtactg ctgcaatgag 1260
301 cacgagtgcc accatcgcta tgctgagtta tatgtgattg atgtcaatat caatatatca 1320
303 tgtgaaactg atgggtactt aactaaaatg acttgcagat ggtcaaccaa tgcaatccaa 1380
305 tcaacttgtg gaagcacttt gcagttgagg tatcatagga gtagcctcta ctgttctgac 1440
307 gttccatctg tgcaccccat atctgaaccc aaagattgcc agttgcagag agatggtttt 1500
309 tatgaatgca tatttcagcc aatatttctg ctatctggct atacaatgtg gattagaata 1560
311 aatcacccgt tgggttctact tgattctcca ccaacatgtg tcattcctga ttccgtgggtg 1620
313 aaaccgctgc ctccatccag tgtgaaagca gaaattactg caaaaattgg attactgaaa 1680
315 atatcttggg agaagccagt cttcccagag aataatcttc agttccagat tcgctatggg 1740
317 ttaagtggaa aagaagtaca gtggaagatc tatgagggtat atgacacaaa gttaaaatcc 1800
319 accagtctcc cggtgccaga cctgtgtgca gtctatgctg tccaggtgcg ctgtaagagg 1860
321 ctagatggac tgggctattg gagtaattgg agtactccag cctacacagt tgtcacggat 1920
323 gtaaaagtgc ctatcagagg acctgaattt tggagaataa ttaatgaaga tgccactaaa 1980
325 aaagagagga atatcactct gctctggaag cctctgatga aaaatgactc attgtgcagc 2040
327 gtgagaagtt atgtggtgaa acatcatact tcccgccatg gaacatgggc agaagatgtg 2100
329 ggaaaccaca ctaaactcac ttctcttggg acagagcaag cacattctgt tacagttctg 2160
331 gccgtcaatt caattgggtgc ttcttcgcga aattttaatt taacattctc atggccccatg 2220
333 agcaaagtaa atatcgtgca gtcgctcagt gcttatcctt taaacagcag ttgtgtgggt 2280
335 ctttcctggc tgctctcacc cagtgattac aatctgatgt attttattct tgagtggaaa 2340
337 attcttaatg aagaccatga aattaaatgg ctccagaatcc cttcctctgt taaaaagtat 2400
339 tatatccacg atcattttat tcctattgag aaatatcaat tcagtcttta ccccatattc 2460
341 atggaaggag tggggaaacc gaagataatt aacagtttca cccaagatgg tgaaaaacac 2520
343 cggaatgatg caggtctata tgtaattgtg ccaataatta ttctctctc aatcttattg 2580
345 cttggaacat tgtaaatgtc acaccaaaga atgaaaaagc tattttggga agatgttcca 2640
347 aacccaaga actgttctctg ggcacaagga cttaattttc agaagccgga aacatttgag 2700
349 catcttttta tcaagcacac agaatcagtg acatttggcc ctctctcttt ggagcctgaa 2760
351 accatttcag aagatatcag tgttgataca tcatggaaaa ataaggatga gatggtgcca 2820
353 ccaactacag tctctctact cttgacaact ccggaccttg aaaagagttc aatttgtatt 2880
355 agtgaccaac gcagcagtg cacttctct gaggtgaga gcatggagat aactcgtgag 2940
357 gatgaaaata gaagacagcc ctctattaaa tatgccacc tgctcagcag ccctaaatca 3000
359 ggtgaaactg agcaagagca agaacttgta agtagcttg tcagcagatg cttctctagc 3060
361 agcaattccc taccgaaaga gtctttctcg aatagctcat gggagataga aaccaggcc 3120
363 ttttttattt tatcagatca gcatcccaat atgacttcac cacacctttc cttctcagaa 3180
365 ggattggatg aacttatgaa gtttgaggga aatttcccca aagaacataa tgacgaaagg 3240
367 tctgtctatt atttaggagt cacctcaatc aaaaagagag agagtgatgt gtttttgact 3300
369 gatgagtcaa gagtgcggtg cccattccca gccactggtt tattcgctga catcaaaatc 3360
371 ctccaggaga gctgttcaca ccttgtagaa aataatttca atttaggaaac ttctgggtcag 3420
373 aagacttttg tatcttacat gcctcaattt caaacttggt caactcagac tcagaagata 3480
375 atggaaaaca agatgtatga cctaaccgtc taagttcatt ccagaaacat ctcagattta 3540
377 tgatgggatg agtcatatta agggtaatat gttctacatg gtgttccata gcagagagaa 3600
379 aaaaattgag tcaaatttga aaatgacttc aaaagttaaa gagatctgtt tgtccacact 3660
381 cagtaataca gaaaaaaaaa tgtgagaaag ccttcaagag cctagtaatg tagacctact 3720
383 cttctaataa ttctcttaac cggctacagt gggagttct cgaatgcctt gtgtctagct 3780
385 agaaacaagc ccaacaatac tagcgttttg agcattaatc tcatgtagaa agagctaatac 3840
387 catctgaatt acacatacat ctgaaagaag acttcagact aacacttggt aaatgtaatg 3900
389 tcttcaagag tgtgattgtt ttatcttgag gtgtctttgt ttacactaa ttacacata 3960
391 cacatatgca cacttgtatc taataggtat cctgtacatt gttaaatata tgatgtactt 4020
393 gtttttgtgc taaaaaaaaa aaaaaaaaaa 4050

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; N Pos. 299,310,311
Seq#:10; Xaa Pos. 56,60
Seq#:11; Xaa Pos. 56,60
Seq#:13; N Pos. 425,428,429,430,484,485,498,499,527,528,567,568,579,580,586
Seq#:13; N Pos. 587,588,595,596,597,599,600,602,603,604,605,606,608,610,611
Seq#:13; N Pos. 612,613,614,615,616,617,618,619,620,621,622,623,641,642,643
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Seq#:13; N Pos. 670,671,672,673,674,675,676,677,678,679,680,681,682,683,685
Seq#:13; N Pos. 686,687,691,692,693,694,695,696,697,698,699,700,701,702,703
Seq#:13; N Pos. 704,706,707,709,710,711,712,713,714,715,716,717,718,719,720
Seq#:13; N Pos. 721,722,723,724,725,726,727,728,729,730,731,732,733,734,735
Seq#:13; N Pos. 736,737,738,739,740,741,742,743,744,745,746,747,748,749,750
Seq#:13; N Pos. 751,752,753,754,755,756,757,758,759,760,761,762,763,764,765
Seq#:13; N Pos. 766,767,768,769,770,771,772,773,774,775,776,777,778,779,780
Seq#:13; N Pos. 781,782,783,784,785,786,787,788,789,790,791,792,793,794,795
Seq#:13; N Pos. 796,797,798,799,800,801,802,803,804,805,806,807,808,809,810
Seq#:13; N Pos. 811,812,813,814,815,816,817,818,819,820,821,822,823,824,825
Seq#:13; N Pos. 826,827,828,829,830,831,832,833,834,835,836,837,838,839,840
Seq#:13; N Pos. 841,842,843,844,845,846,847,848,849,850,851,852,853,854,858
Seq#:13; N Pos. 859,861,867,868,869,870,871,872,876,878,879,880,881,882,883
Seq#:13; N Pos. 885
Seq#:14; N Pos. 403,404,407,408,409,418,419,420,432,433,434,435,436,442,443
Seq#:14; N Pos. 444,445
Seq#:15; N Pos. 658,659,660,667,668,669,670,671,673,674,675,682,689,690,691
Seq#:15; N Pos. 692,693,696,697,698,699,700,702,731,732,739,745,746,751,752
Seq#:15; N Pos. 753,755,756,758,759,760,764,767,768,770
Seq#:42; N Pos. 103
Seq#:43; N Pos. 192

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:267
M:341 Repeated in SeqNo=10
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:48
L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:420
M:341 Repeated in SeqNo=13
L:469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:360
M:341 Repeated in SeqNo=14
L:506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:600
M:341 Repeated in SeqNo=15
L:865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:60
L:896 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:180